



SEQUENCE LISTING

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<120> METHODS FOR IDENTIFYING AGENTS WHICH ALTER HISTONE
PROTEIN ACETYLATION, DECREASE AGING, INCREASE LIFESPAN

<130> 13407-016002

<140> US 09/735,786

<141> 2000-12-13

<150> US 09/461,580

<151> 1999-12-15

<160> 38

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 737

<212> PRT

<213> Mus musculus

<400> 1

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Ala Ala Ala Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu
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Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly
35 40 45
Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala
50 55 60
Ser Ala Ala Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala
65 70 75 80
Ala Ser Ala Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly
85 90 95
Asp Asn Gly Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe
100 105 110
Asp Asp Asp Glu Gly Glu Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala
115 120 125
Ala Ala Ala Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu
130 135 140
Leu Thr Asn Gly Phe His Ser Cys Glu Ser Asp Asp Asp Asp Arg Thr
145 150 155 160
Ser His Ala Ser Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro
165 170 175
Tyr Thr Phe Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr
180 185 190
Ile Leu Lys Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp
195 200 205
Asp Met Thr Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro
210 215 220

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TECH CENTER 1600/2900

Lys	Arg	Lys	Lys	Arg	Lys	Asp	Ile	Asn	Thr	Ile	Glu	Asp	Ala	Val	Lys
225					230					235					240
Leu	Leu	Gln	Glu	Cys	Lys	Lys	Ile	Ile	Val	Leu	Thr	Gly	Ala	Gly	Val
				245					250					255	
Ser	Val	Ser	Cys	Gly	Ile	Pro	Asp	Phe	Arg	Ser	Arg	Asp	Gly	Ile	Tyr
			260					265					270		
Ala	Arg	Leu	Ala	Val	Asp	Phe	Pro	Asp	Leu	Pro	Asp	Pro	Gln	Ala	Met
			275				280					285			
Phe	Asp	Ile	Glu	Tyr	Phe	Arg	Lys	Asp	Pro	Arg	Pro	Phe	Phe	Lys	Phe
	290					295				300					
Ala	Lys	Glu	Ile	Tyr	Pro	Gly	Gln	Phe	Gln	Pro	Ser	Leu	Cys	His	Lys
305					310					315					320
Phe	Ile	Ala	Leu	Ser	Asp	Lys	Glu	Gly	Lys	Leu	Leu	Arg	Asn	Tyr	Thr
				325					330					335	
Gln	Asn	Ile	Asp	Thr	Leu	Glu	Gln	Val	Ala	Gly	Ile	Gln	Arg	Ile	Leu
			340					345					350		
Gln	Cys	His	Gly	Ser	Phe	Ala	Thr	Ala	Ser	Cys	Leu	Ile	Cys	Lys	Tyr
		355					360					365			
Lys	Val	Asp	Cys	Glu	Ala	Val	Arg	Gly	Asp	Ile	Phe	Asn	Gln	Val	Val
	370					375					380				
Pro	Arg	Cys	Pro	Arg	Cys	Pro	Ala	Asp	Glu	Pro	Leu	Ala	Ile	Met	Lys
385					390					395					400
Pro	Glu	Ile	Val	Phe	Phe	Gly	Glu	Asn	Leu	Pro	Glu	Gln	Phe	His	Arg
				405				410						415	
Ala	Met	Lys	Tyr	Asp	Lys	Asp	Glu	Val	Asp	Leu	Leu	Ile	Val	Ile	Gly
			420				425					430			
Ser	Ser	Leu	Lys	Val	Arg	Pro	Val	Ala	Leu	Ile	Pro	Ser	Ser	Ile	Pro
		435				440					445				
His	Glu	Val	Pro	Gln	Ile	Leu	Ile	Asn	Arg	Glu	Pro	Leu	Pro	His	Leu
	450					455					460				
His	Phe	Asp	Val	Glu	Leu	Leu	Gly	Asp	Cys	Asp	Val	Ile	Ile	Asn	Glu
465					470					475					480
Leu	Cys	His	Arg	Leu	Gly	Gly	Glu	Tyr	Ala	Lys	Leu	Cys	Cys	Asn	Pro
				485					490					495	
Val	Lys	Leu	Ser	Glu	Ile	Thr	Glu	Lys	Pro	Pro	Arg	Pro	Gln	Lys	Glu
		500						505					510		
Leu	Val	His	Leu	Ser	Glu	Leu	Pro	Thr	Pro	Leu	His	Ile	Ser	Glu	
		515					520				525				
Asp	Ser	Ser	Ser	Pro	Glu	Arg	Thr	Val	Pro	Gln	Asp	Ser	Ser	Val	Ile
	530					535					540				
Ala	Thr	Leu	Val	Asp	Gln	Ala	Thr	Asn	Asn	Asn	Val	Asn	Asp	Leu	Glu
545					550					555					560
Val	Ser	Glu	Ser	Ser	Cys	Val	Glu	Glu	Lys	Pro	Gln	Glu	Val	Gln	Thr
				565					570					575	
Ser	Arg	Asn	Val	Glu	Asn	Ile	Asn	Val	Glu	Asn	Pro	Asp	Phe	Lys	Ala
			580					585					590		
Val	Gly	Ser	Ser	Thr	Ala	Asp	Lys	Asn	Glu	Arg	Thr	Ser	Val	Ala	Glu
		595					600					605			
Thr	Val	Arg	Lys	Cys	Trp	Pro	Asn	Arg	Leu	Ala	Lys	Glu	Gln	Ile	Ser
	610					615					620				
Lys	Arg	Leu	Glu	Gly	Asn	Gln	Tyr	Leu	Phe	Val	Pro	Pro	Asn	Arg	Tyr
625					630					635					640
Ile	Phe	His	Gly	Ala	Glu	Val	Tyr	Ser	Asp	Ser	Glu	Asp	Asp	Val	Leu
				645					650					655	
Ser	Ser	Ser	Ser	Cys	Gly	Ser	Asn	Ser	Asp	Ser	Gly	Thr	Cys	Gln	Ser
			660					665					670		
Pro	Ser	Leu	Glu	Glu	Pro	Leu	Glu	Asp	Glu	Ser	Glu	Ile	Glu	Glu	Phe

		675					680					685					
Tyr	Asn	Gly	Leu	Glu	Asp	Asp	Thr	Glu	Arg	Pro	Glu	Cys	Ala	Gly	Gly		
	690					695					700						
Ser	Gly	Phe	Gly	Ala	Asp	Gly	Gly	Asp	Gln	Glu	Val	Val	Asn	Glu	Ala		
705					710					715					720		
Ile	Ala	Thr	Arg	Gln	Glu	Leu	Thr	Asp	Val	Asn	Tyr	Pro	Ser	Asp	Lys		
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Ser																	

<210> 2
 <211> 272
 <212> PRT
 <213> *Saccharomyces cerevisiae*

Ile	Asn	Lys	Val	Leu	Cys	Thr	Arg	Leu	Arg	Leu	Ser	Asn	Phe	Phe	Thr		
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Ile	Asp	His	Phe	Ile	Gln	Lys	Leu	His	Thr	Ala	Arg	Lys	Ile	Leu	Val		
			20					25					30				
Leu	Thr	Gly	Ala	Gly	Val	Ser	Thr	Ser	Leu	Gly	Ile	Pro	Asp	Phe	Arg		
		35					40					45					
Ser	Ser	Glu	Gly	Phe	Tyr	Ser	Lys	Ile	Lys	His	Leu	Gly	Leu	Asp	Asp		
	50					55					60						
Pro	Gln	Asp	Val	Phe	Asn	Tyr	Asn	Ile	Phe	Met	His	Asp	Pro	Ser	Val		
65					70				75						80		
Phe	Tyr	Asn	Ile	Ala	Asn	Met	Val	Leu	Pro	Pro	Glu	Lys	Ile	Tyr	Ser		
				85				90						95			
Pro	Leu	His	Ser	Phe	Ile	Lys	Met	Leu	Gln	Met	Lys	Gly	Lys	Leu	Leu		
			100					105					110				
Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	Glu	Ser	Tyr	Ala	Gly	Ile		
	115						120					125					
Ser	Thr	Asp	Lys	Leu	Val	Gln	Cys	His	Gly	Ser	Phe	Ala	Thr	Ala	Thr		
	130					135					140						
Cys	Val	Thr	Cys	His	Trp	Asn	Leu	Pro	Gly	Glu	Arg	Ile	Phe	Asn	Lys		
145					150					155					160		
Ile	Arg	Asn	Leu	Glu	Leu	Pro	Leu	Cys	Pro	Tyr	Cys	Tyr	Lys	Lys	Arg		
			165					170						175			
Arg	Glu	Tyr	Phe	Pro	Glu	Gly	Tyr	Asn	Asn	Lys	Val	Gly	Val	Ala	Ala		
			180					185					190				
Ser	Gln	Gly	Ser	Met	Ser	Glu	Arg	Pro	Pro	Tyr	Ile	Leu	Asn	Ser	Tyr		
		195					200					205					
Gly	Val	Leu	Lys	Pro	Asp	Ile	Thr	Phe	Phe	Gly	Glu	Ala	Leu	Pro	Asn		
	210					215					220						
Lys	Phe	His	Lys	Ser	Ile	Arg	Glu	Asp	Ile	Leu	Glu	Cys	Asp	Leu	Leu		
225					230					235					240		
Ile	Cys	Ile	Gly	Thr	Ser	Leu	Lys	Val	Ala	Pro	Val	Ser	Glu	Ile	Val		
				245					250					255			
Asn	Met	Val	Pro	Ser	His	Val	Pro	Gln	Val	Leu	Ile	Asn	Arg	Asp	Pro		
			260					265					270				

<210> 3
 <211> 267
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 3

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Ile Asn Lys Val Leu Ser Thr Arg Leu Arg Leu Pro Asn Phe Asn Thr
 1          5          10          15
Ile Asp His Phe Thr Ala Thr Leu Arg Asn Ala Lys Lys Ile Leu Val
          20          25          30
Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro Asp Phe Arg
          35          40          45
Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly Leu Glu Asp
          50          55          60
Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp Pro Ser Val
65          70          75          80
Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn Met Tyr Ser
          85          90          95
Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly Lys Leu Leu
          100          105          110
Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr Ala Gly Ile
          115          120          125
Asp Pro Asp Lys Leu Val Gln Cys His Gly Ser Phe Ala Thr Ala Ser
          130          135          140
Cys Val Thr Cys His Trp Gln Ile Pro Gly Glu Lys Ile Phe Glu Asn
145          150          155          160
Ile Arg Asn Leu Glu Leu Pro Leu Cys Pro Tyr Cys Tyr Gln Lys Arg
          165          170          175
Lys Gln Tyr Phe Pro Met Ser Asn Gly Asn Asn Thr Val Gln Thr Asn
          180          185          190
Ile Asn Phe Asn Ser Pro Ile Leu Lys Ser Tyr Gly Val Leu Lys Pro
          195          200          205
Asp Met Thr Phe Phe Gly Glu Ala Leu Pro Ser Arg Phe His Lys Thr
          210          215          220
Ile Arg Lys Asp Ile Leu Glu Cys Asp Leu Leu Ile Cys Ile Gly Thr
225          230          235          240
Ser Leu Lys Val Ala Pro Val Ser Glu Ile Val Asn Met Val Pro Ser
          245          250          255
His Val Pro Gln Ile Leu Ile Asn Arg Asp Met
          260          265

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<210> 4

<211> 245

<212> PRT

<213> Mus musculus

<400> 4

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Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys Lys Arg Lys Asp
 1          5          10          15
Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln Glu Cys Lys Lys
          20          25          30
Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser Cys Gly Ile Pro
          35          40          45
Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu Ala Val Asp Phe
          50          55          60
Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile Glu Tyr Phe Arg
65          70          75          80
Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu Ile Tyr Pro Gly
          85          90          95
Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala Leu Ser Asp Lys
          100          105          110
Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Thr Leu Glu
          115          120          125

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Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His Gly Ser Phe Ala
 130 135 140
 Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp Cys Glu Ala Val
 145 150 155 160
 Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys Pro Arg Cys Pro
 165 170 175
 Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile Val Phe Phe Gly
 180 185 190
 Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys Tyr Asp Lys Asp
 195 200 205
 Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu Lys Val Arg Pro
 210 215 220
 Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val Pro Gln Ile Leu
 225 230 235 240
 Ile Asn Arg Glu Pro
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<210> 5

<211> 237

<212> PRT

<213> Salmonella typhimurium

<400> 5

Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser
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 Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu
 20 25 30
 Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Phe Ala Arg Asn
 35 40 45
 Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln
 50 55 60
 Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu
 65 70 75 80
 Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp
 85 90 95
 Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly
 100 105 110
 Glu Leu Leu Lys Val Arg Cys Ser Gln Ser Gly Gln Ile Leu Glu Trp
 115 120 125
 Asn Gly Asp Val Met Pro Glu Asp Lys Cys His Cys Cys Gln Phe Pro
 130 135 140
 Ala Pro Leu Arg Pro His Val Val Trp Phe Gly Glu Met Pro Leu Gly
 145 150 155 160
 Met Asp Glu Ile Tyr Met Ala Leu Ser Met Ala Asp Ile Phe Ile Ala
 165 170 175
 Ile Gly Thr Ser Gly His Val Tyr Pro Ala Ala Gly Phe Val His Glu
 180 185 190
 Ala Lys Leu His Gly Ala His Thr Val Glu Leu Asn Leu Glu Pro Ser
 195 200 205
 Gln Val Gly Asn Glu Phe Glu Glu Lys His Tyr Gly Pro Ala Ser Gln
 210 215 220
 Val Val Pro Glu Phe Val Asp Lys Phe Leu Lys Gly Leu
 225 230 235

<210> 6

<211> 21

<212> PRT

<213> Homo sapiens

<400> 6

Ala	Arg	Thr	Lys	Gln	Thr	Ala	Arg	Lys	Ser	Thr	Gly	Gly	Lys	Ala	Pro
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Arg	Lys	Gln	Leu	Cys											
			20												

<210> 7

<211> 20

<212> PRT

<213> Homo sapiens

<400> 7

Ser	Gly	Arg	Gly	Lys	Gly	Gly	Lys	Gly	Leu	Gly	Lys	Gly	Gly	Ala	Lys
1				5					10					15	
Arg	His	Arg	Cys												
			20												

<210> 8

<211> 19

<212> PRT

<213> Homo sapiens

<400> 8

Ala	Gly	Gly	Lys	Gly	Gly	Lys	Gly	Met	Gly	Lys	Val	Gly	Ala	Lys	Arg
1				5					10					15	
His	Ser	Cys													

<210> 9

<211> 128

<212> PRT

<213> Mus musculus

<400> 9

Ile	Val	Leu	Thr	Gly	Ala	Gly	Val	Ser	Val	Ser	Cys	Gly	Ile	Pro	Asp
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Phe	Arg	Ser	Arg	Asp	Gly	Ile	Tyr	Ala	Arg	Leu	Ala	Val	Asp	Phe	Pro
			20				25					30			
Asp	Leu	Pro	Asp	Pro	Gln	Ala	Met	Phe	Asp	Ile	Glu	Tyr	Phe	Arg	Lys
		35					40				45				
Asp	Pro	Arg	Pro	Phe	Phe	Lys	Phe	Ala	Lys	Glu	Ile	Tyr	Pro	Gly	Gln
	50					55					60				
Phe	Gln	Pro	Ser	Leu	Cys	His	Lys	Phe	Ile	Ala	Leu	Ser	Asp	Lys	Glu
65					70					75				80	
Gly	Lys	Leu	Leu	Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Thr	Leu	Glu	Gln
				85					90					95	
Val	Ala	Gly	Ile	Gln	Arg	Ile	Leu	Gln	Cys	His	Gly	Ser	Phe	Ala	Thr
			100					105					110		
Ala	Ser	Cys	Leu	Ile	Cys	Lys	Tyr	Lys	Val	Asp	Cys	Glu	Ala	Val	Arg
		115					120					125			

<210> 10

<211> 128

<212> PRT

<213> Saccharomyces cerevisiae

<400> 10

Leu	Val	Leu	Thr	Gly	Ala	Gly	Val	Ser	Thr	Ser	Leu	Gly	Ile	Pro	Asp
1				5					10					15	
Phe	Arg	Ser	Ser	Glu	Gly	Phe	Tyr	Ser	Lys	Ile	Lys	His	Leu	Gly	Leu
			20					25					30		
Asp	Asp	Pro	Gln	Asp	Val	Phe	Asn	Tyr	Asn	Ile	Phe	Met	His	Asp	Pro
		35					40					45			
Ser	Val	Phe	Tyr	Asn	Ile	Ala	Asn	Met	Val	Leu	Pro	Pro	Glu	Lys	Ile
	50					55					60				
Tyr	Ser	Pro	Leu	His	Ser	Phe	Ile	Lys	Met	Leu	Gln	Met	Lys	Gly	Lys
65					70				75						80
Leu	Leu	Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	Glu	Ser	Tyr	Ala
			85					90						95	
Gly	Ile	Ser	Thr	Asp	Lys	Leu	Val	Gln	Cys	His	Gly	Ser	Phe	Ala	Thr
			100					105					110		
Ala	Thr	Cys	Val	Thr	Cys	His	Trp	Asn	Leu	Pro	Gly	Glu	Arg	Ile	Phe
		115					120					125			

<210> 11

<211> 336

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 11

Ala	Ile	Asn	Lys	Val	Leu	Cys	Thr	Arg	Leu	Arg	Leu	Ser	Asn	Phe	Phe
1				5					10					15	
Thr	Ile	Asp	His	Phe	Ile	Gln	Lys	Leu	His	Thr	Ala	Arg	Lys	Ile	Leu
			20					25					30		
Val	Leu	Thr	Gly	Ala	Gly	Val	Ser	Thr	Ser	Leu	Gly	Ile	Pro	Asp	Phe
		35				40					45				
Arg	Ser	Ser	Glu	Gly	Phe	Tyr	Ser	Lys	Ile	Lys	His	Leu	Gly	Leu	Asp
	50				55					60					
Asp	Pro	Gln	Asp	Val	Phe	Asn	Tyr	Asn	Ile	Phe	Met	His	Asp	Pro	Ser
65				70					75					80	
Val	Phe	Tyr	Asn	Ile	Ala	Asn	Met	Val	Leu	Pro	Pro	Glu	Lys	Ile	Tyr
			85					90						95	
Ser	Pro	Leu	His	Ser	Phe	Ile	Lys	Met	Leu	Gln	Met	Lys	Gly	Lys	Leu
			100				105						110		
Leu	Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Asn	Leu	Glu	Ser	Tyr	Ala	Gly
		115					120					125			
Ile	Ser	Thr	Asp	Lys	Leu	Val	Gln	Cys	His	Gly	Ser	Phe	Ala	Thr	Ala
	130					135					140				
Thr	Cys	Val	Thr	Cys	His	Trp	Asn	Leu	Pro	Gly	Glu	Arg	Ile	Phe	Asn
145				150						155				160	
Lys	Ile	Arg	Asn	Leu	Glu	Leu	Pro	Leu	Cys	Pro	Tyr	Cys	Tyr	Lys	Lys
			165					170						175	
Arg	Arg	Glu	Tyr	Phe	Pro	Glu	Gly	Tyr	Asn	Asn	Lys	Val	Gly	Val	Ala
			180				185						190		
Ala	Ser	Gln	Gly	Ser	Met	Ser	Glu	Arg	Pro	Pro	Tyr	Ile	Leu	Asn	Ser
	195					200						205			
Tyr	Gly	Val	Leu	Lys	Pro	Asp	Ile	Thr	Phe	Phe	Gly	Glu	Ala	Leu	Pro
	210				215						220				
Asn	Lys	Phe	His	Lys	Ser	Ile	Arg	Glu	Asp	Ile	Leu	Glu	Cys	Asp	Leu
225				230					235					240	
Leu	Ile	Cys	Ile	Gly	Thr	Ser	Leu	Lys	Val	Ala	Pro	Val	Ser	Glu	Ile
			245					250						255	

Val	Asn	Met	Val	Pro	Ser	His	Val	Pro	Gln	Val	Leu	Ile	Asn	Arg	Asp
		260						265					270		
Pro	Val	Lys	His	Ala	Glu	Phe	Asp	Leu	Ser	Leu	Leu	Gly	Tyr	Cys	Asp
		275					280					285			
Asp	Ile	Ala	Ala	Met	Val	Ala	Gln	Lys	Cys	Gly	Trp	Thr	Ile	Pro	His
	290					295					300				
Lys	Lys	Trp	Asn	Asp	Leu	Lys	Asn	Lys	Asn	Phe	Lys	Cys	Gln	Glu	Lys
305					310					315				320	
Asp	Lys	Gly	Val	Tyr	Val	Val	Thr	Ser	Asp	Glu	His	Pro	Lys	Thr	Leu
			325						330					335	

<210> 12

<211> 327

<212> PRT

<213> Mus musculus

<400> 12

Val	Ile	Asn	Ile	Leu	Ser	Glu	Pro	Pro	Lys	Arg	Lys	Lys	Arg	Lys	Asp
1				5					10					15	
Ile	Asn	Thr	Ile	Glu	Asp	Ala	Val	Lys	Leu	Leu	Gln	Glu	Cys	Lys	Lys
			20					25					30		
Ile	Ile	Val	Leu	Thr	Gly	Ala	Gly	Val	Ser	Val	Ser	Cys	Gly	Ile	Pro
		35				40						45			
Asp	Phe	Arg	Ser	Arg	Asp	Gly	Ile	Tyr	Ala	Arg	Leu	Ala	Val	Asp	Phe
	50					55					60				
Pro	Asp	Leu	Pro	Asp	Pro	Gln	Ala	Met	Phe	Asp	Ile	Glu	Tyr	Phe	Arg
65					70					75					80
Lys	Asp	Pro	Arg	Pro	Phe	Phe	Lys	Phe	Ala	Lys	Glu	Ile	Tyr	Pro	Gly
				85					90					95	
Gln	Phe	Gln	Pro	Ser	Leu	Cys	His	Lys	Phe	Ile	Ala	Leu	Ser	Asp	Lys
			100					105					110		
Glu	Gly	Lys	Leu	Leu	Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Thr	Leu	Glu
	115						120					125			
Gln	Val	Ala	Gly	Ile	Gln	Arg	Ile	Leu	Gln	Cys	His	Gly	Ser	Phe	Ala
	130					135					140				
Thr	Ala	Ser	Cys	Leu	Ile	Cys	Lys	Tyr	Lys	Val	Asp	Cys	Glu	Ala	Val
145					150					155					160
Arg	Gly	Asp	Ile	Phe	Asn	Gln	Val	Val	Pro	Arg	Cys	Pro	Arg	Cys	Pro
				165					170					175	
Ala	Asp	Glu	Pro	Leu	Ala	Ile	Met	Lys	Pro	Glu	Ile	Val	Phe	Phe	Gly
			180					185					190		
Glu	Asn	Leu	Pro	Glu	Gln	Phe	His	Arg	Ala	Met	Lys	Tyr	Asp	Lys	Asp
	195						200					205			
Glu	Val	Asp	Leu	Leu	Ile	Val	Ile	Gly	Ser	Ser	Leu	Lys	Val	Arg	Pro
	210					215					220				
Val	Ala	Leu	Ile	Pro	Ser	Ser	Ile	Pro	His	Glu	Val	Pro	Gln	Ile	Leu
225					230					235					240
Ile	Asn	Arg	Glu	Pro	Leu	Pro	His	Leu	His	Phe	Asp	Val	Glu	Leu	Leu
				245					250					255	
Gly	Asp	Cys	Asp	Val	Ile	Ile	Asn	Glu	Leu	Cys	His	Arg	Leu	Gly	Gly
			260					265					270		
Glu	Tyr	Ala	Lys	Leu	Cys	Cys	Asn	Pro	Val	Lys	Leu	Ser	Glu	Ile	Thr
	275						280					285			
Glu	Lys	Pro	Pro	Arg	Pro	Gln	Lys	Glu	Leu	Val	His	Leu	Ser	Glu	Leu
	290					295					300				
Pro	Pro	Thr	Pro	Leu	His	Ile	Ser	Glu	Asp	Ser	Ser	Ser	Pro	Glu	Arg
305					310					315					320

Thr Val Pro Gln Asp Ser Ser
325

<210> 13
<211> 237
<212> PRT
<213> Salmonella typhimurium

<400> 13
Met Met Glu Asn Pro Arg Val Leu Val Leu Thr Gly Ala Gly Ile Ser
1 5 10 15
Ala Glu Ser Gly Ile Arg Thr Phe Arg Ala Ala Asp Gly Leu Trp Glu
20 25 30
Glu His Arg Val Glu Asp Val Ala Thr Pro Glu Gly Pro Ala Arg Asn
35 40 45
Pro Gly Leu Val Gln Thr Phe Tyr Asn Ala Arg Arg Gln Gln Leu Gln
50 55 60
Gln Pro Glu Ile Gln Pro Asn Ala Ala His Leu Ala Leu Ala Asn Leu
65 70 75 80
Lys Lys Arg Leu Ala Ile Ala Phe Leu Leu Val Thr Gln Asn Ile Asp
85 90 95
Asn Leu His Glu Arg Ala Gly Asn Arg Asn Ile Ile Gln Met His Gly
100 105 110
Glu Leu Leu Lys Val Arg Cys Ser Gln Ser Gly Gln Ile Leu Glu Trp
115 120 125
Asn Gly Asp Val Met Pro Glu Asp Lys Cys His Cys Cys Gln Phe Pro
130 135 140
Ala Pro Leu Arg Pro His Val Val Trp Phe Gly Glu Met Pro Leu Gly
145 150 155 160
Met Asp Glu Ile Tyr Met Ala Leu Ser Met Ala Asp Ile Phe Ile Ala
165 170 175
Ile Gly Thr Ser Gly His Val Tyr Pro Ala Ala Gly Phe Val His Glu
180 185 190
Ala Lys Leu His Gly Ala His Thr Val Glu Leu Asn Leu Glu Pro Ser
195 200 205
Gln Val Gly Asn Glu Phe Glu Lys His Tyr Gly Pro Ala Ser Gln
210 215 220
Val Val Pro Glu Phe Val Asp Lys Phe Leu Lys Gly Leu
225 230 235

<210> 14
<211> 106
<212> PRT
<213> Saccharomyces cerevisiae

<400> 14
Ile Leu Val Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro
1 5 10 15
Asp Phe Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Lys His Leu Gly
20 25 30
Leu Asp Asp Pro Gln Asp Val Phe Asn Tyr Asn Ile Phe Met His Asp
35 40 45
Pro Ser Val Phe Tyr Asn Ile Ala Asn Met Val Leu Pro Pro Glu Lys
50 55 60
Ile Tyr Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Met Lys Gly
65 70 75 80
Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr

				85				90			95
Ala	Gly	Ile	Ser	Thr	Asp	Lys	Leu	Val	Gln		
			100					105			

<210> 15
 <211> 106
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 15
 Ile Leu Val Leu Thr Gly Ala Gly Val Ser Thr Ser Leu Gly Ile Pro
 1 5 10 15
 Asp Phe Arg Ser Ser Glu Gly Phe Tyr Ser Lys Ile Arg His Leu Gly
 20 25 30
 Leu Glu Asp Pro Gln Asp Val Phe Asn Leu Asp Ile Phe Leu Gln Asp
 35 40 45
 Pro Ser Val Phe Tyr Asn Ile Ala His Met Val Leu Pro Pro Glu Asn
 50 55 60
 Met Tyr Ser Pro Leu His Ser Phe Ile Lys Met Leu Gln Asp Lys Gly
 65 70 75 80
 Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile Asp Asn Leu Glu Ser Tyr
 85 90 95
 Ala Gly Ile Asp Pro Asp Lys Leu Val Gln
 100 105

<210> 16
 <211> 107
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 16
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 1 5 10 15
 Asp Phe Arg Ser Pro Gly Thr Gly Leu Tyr His Asn Leu Ala Arg Leu
 20 25 30
 Lys Leu Pro Tyr Pro Glu Ala Val Phe Asp Val Asp Phe Phe Gln Ser
 35 40 45
 Asp Pro Leu Pro Phe Tyr Thr Leu Ala Lys Glu Leu Tyr Pro Gly Asn
 50 55 60
 Phe Arg Pro Ser Lys Phe His Tyr Leu Leu Lys Leu Phe Gln Asp Lys
 65 70 75 80
 Asp Val Leu Lys Arg Val Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg
 85 90 95
 Gln Ala Gly Val Lys Asp Asp Leu Ile Ile Glu
 100 105

<210> 17
 <211> 131
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 17
 Ile Ala Cys Leu Thr Gly Ala Gly Ile Ser Cys Asn Ala Gly Ile Pro
 1 5 10 15
 Asp Phe Arg Ser Ser Asp Gly Leu Tyr Asp Leu Val Lys Lys Asp Cys
 20 25 30
 Ser Gln Tyr Trp Ser Ile Lys Ser Gly Arg Glu Met Phe Asp Ile Ser

[illegible]

<210> 18

<211> 117

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

[illegible]

<210> 19

<211> 106

<212> PRT

<213> Mus musculus

<400> 19

Ile	Ile	Val	Leu	Thr	Gly	Ala	Gly	Val	Ser	Val	Ser	Cys	Gly	Ile	Pro
1				5					10					15	
Asp	Phe	Arg	Ser	Arg	Asp	Gly	Ile	Tyr	Ala	Arg	Leu	Ala	Val	Asp	Phe
			20					25					30		
Pro	Asp	Leu	Pro	Asp	Pro	Gln	Ala	Met	Phe	Asp	Ile	Glu	Tyr	Phe	Arg
		35					40					45			
Lys	Asp	Pro	Arg	Pro	Phe	Phe	Lys	Phe	Ala	Lys	Glu	Ile	Tyr	Pro	Gly
	50					55					60				
Gln	Phe	Gln	Pro	Ser	Leu	Cys	His	Lys	Phe	Ile	Ala	Leu	Ser	Asp	Lys
65					70					75				80	
Glu	Gly	Lys	Leu	Leu	Arg	Asn	Tyr	Thr	Gln	Asn	Ile	Asp	Thr	Leu	Glu
				85					90					95	
Gln	Val	Ala	Gly	Ile	Gln	Arg	Ile	Leu	Gln						
			100					105							

<210> 20
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 20
 Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro
 1 5 10 15
 Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Ala Asn Leu Glu Lys Tyr
 20 25 30
 His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys
 35 40 45
 His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln
 50 55 60
 Phe Lys Pro Thr Ile Cys His Tyr Phe Ile Arg Leu Leu Lys Glu Lys
 65 70 75 80
 Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg
 85 90 95
 Val Ala Gly Leu Glu Pro Gln Asp Leu Val Glu
 100 105

<210> 21
 <211> 86
 <212> PRT
 <213> Mus musculus

<400> 21
 Gly Thr Arg Leu Tyr Ser Asn Leu Gln Gln Tyr Asp Ile Pro Tyr Pro
 1 5 10 15
 Glu Ala Ile Phe Glu Leu Gly Phe Phe Phe His Asn Pro Lys Pro Phe
 20 25 30
 Phe Met Leu Ala Lys Glu Leu Tyr Pro Gly His Tyr Arg Pro Asn Val
 35 40 45
 Thr His Tyr Phe Leu Arg Leu His Asp Lys Glu Leu Leu Leu Arg
 50 55 60
 Leu Tyr Thr Gln Asn Ile Asp Gly Leu Glu Arg Ala Ser Gly Ile Pro
 65 70 75 80
 Ala Ser Lys Leu Val Glu
 85

<210> 22
 <211> 85
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown Protein

<400> 22
 Val Val Phe His Thr Gly Ala Gly Ile Ser Thr Ala Ser Gly Ile Pro
 1 5 10 15
 Asp Phe Arg Gly Pro His Gly Val Trp Thr Met Glu Glu Arg Gly Leu
 20 25 30
 Ala Pro Lys Phe Asp Thr Thr Phe Glu Asn Ala Arg Pro Ser Lys Thr
 35 40 45
 His Met Ala Leu Val Gln Leu Glu Arg Met Gly Phe Leu Ser Phe Leu

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      50              55              60
Val Ser Gln Asn Val Asp Gly Leu Asp Val Arg Ser Gly Phe Pro Arg
65              70              75              80
Asp Lys Leu Ala Glu
      85

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<210> 23
 <211> 71
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown Protein

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<400> 23
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1              5              10              15
Asp Tyr Arg Ser Glu Lys Val Gly Leu Tyr Ala Arg Thr Asp Arg Arg
      20              25              30
Pro Ile Gln His Ile Asp Phe Val Pro Val Leu Arg Ser Ala Ser Gly
      35              40              45
Thr Trp Pro Glu Asn Leu Trp Ala Gly Leu Asn Ser Pro Leu Thr Asn
      50              55              60
Pro Thr Gln His Thr Trp Leu
65              70

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<210> 24
 <211> 75
 <212> PRT
 <213> Unknown

<220>
 <223> Unknown Protein

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<400> 24
Ile Ala Ile Ile Ser Gly Ala Gly Val Ser Ala Glu Ser Gly Val Pro
1              5              10              15
Thr Phe Arg Gly Ala Gly Gly Tyr Trp Arg Lys Trp Gln Ala Gln Asp
      20              25              30
Leu Ala Thr Pro Gln Ala Phe Ala Arg Asn Pro Ser Gln Val Trp Glu
      35              40              45
Phe Tyr His Tyr Arg Arg Glu Val Met Arg Ser Lys Glu Pro Asn Pro
      50              55              60
Gly His Leu Ala Ile Ala Gln Cys Glu Ala Arg
65              70              75

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<210> 25
 <211> 3869
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (48)...(2258)

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<400> 25
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Met Ala Asp
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gcc atg gag gcc gcg tcg cag ccg gcg gac gag ccg ctc cgc aag agg Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu Arg Lys Arg 20 25 30 35	152
ccc cgc cga gac ggg cct ggc ctc ggg cgc agc ccg ggc gag ccg agc Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly Glu Pro Ser 40 45 50	200
gca gca gtg gcg ccg gcg gcc gcg ggg tgt gag gcg gcg agc gcc gcg Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala Ser Ala Ala 55 60 65	248
gcc ccg gcg gcg ctg tgg cgg gag gcg gca ggg gcg gcg gcg agc gcg Ala Pro Ala Ala Leu Trp Arg Glu Ala Ala Gly Ala Ala Ala Ser Ala 70 75 80	296
gag cgg gag gcc ccg gcg acg gcc gtg gcc ggg gac gga gac aat ggg Glu Arg Glu Ala Pro Ala Thr Ala Val Ala Gly Asp Gly Asp Asn Gly 85 90 95	344
tcc ggc ctg cgg cgg gag ccg agg gcg gct gac gac ttc gac gac gac Ser Gly Leu Arg Arg Glu Pro Arg Ala Ala Asp Asp Phe Asp Asp Asp 100 105 110 115	392
gag ggc gag gag gag gac gag gcg gcg gcg gca gcg gcg gcg gca gcg Glu Gly Glu Glu Glu Asp Glu Ala Ala Ala Ala Ala Ala Ala Ala Ala 120 125 130	440
atc ggc tac cga gac aac ctc ctg ttg acc gat gga ctc ctc act aat Ile Gly Tyr Arg Asp Asn Leu Leu Leu Thr Asp Gly Leu Leu Thr Asn 135 140 145	488
ggc ttt cat tcc tgt gaa agt gat gac gat gac aga acg tca cac gcc Gly Phe His Ser Cys Glu Ser Asp Asp Asp Asp Arg Thr Ser His Ala 150 155 160	536
agc tct agt gac tgg act ccg cgg ccg cgg ata ggt cca tat act ttt Ser Ser Ser Asp Trp Thr Pro Arg Pro Arg Ile Gly Pro Tyr Thr Phe 165 170 175	584
gtt cag caa cat ctc atg att ggc acc gat cct cga aca att ctt aaa Val Gln Gln His Leu Met Ile Gly Thr Asp Pro Arg Thr Ile Leu Lys 180 185 190 195	632
gat tta tta cca gaa aca att cct cca cct gag ctg gat gat atg acg Asp Leu Leu Pro Glu Thr Ile Pro Pro Pro Glu Leu Asp Asp Met Thr 200 205 210	680
ctg tgg cag att gtt att aat atc ctt tca gaa cca cca aag cgg aaa Leu Trp Gln Ile Val Ile Asn Ile Leu Ser Glu Pro Pro Lys Arg Lys	728

215	220	225	
aaa aga aaa gat atc aat aca att gaa gat gct gtg aag tta ctg cag Lys Arg Lys Asp Ile Asn Thr Ile Glu Asp Ala Val Lys Leu Leu Gln 230 235 240			776
gag tgt aaa aag ata ata gtt ctg act gga gct ggg gtt tct gtc tcc Glu Cys Lys Lys Ile Ile Val Leu Thr Gly Ala Gly Val Ser Val Ser 245 250 255			824
tgt ggg att cct gac ttc aga tca aga gac ggt atc tat gct cgc ctt Cys Gly Ile Pro Asp Phe Arg Ser Arg Asp Gly Ile Tyr Ala Arg Leu 260 265 270 275			872
gcg gtg gac ttc cca gac ctc cca gac cct caa gcc atg ttt gat att Ala Val Asp Phe Pro Asp Leu Pro Asp Pro Gln Ala Met Phe Asp Ile 280 285 290			920
gag tat ttt aga aaa gac cca aga cca ttc ttc aag ttt gca aag gaa Glu Tyr Phe Arg Lys Asp Pro Arg Pro Phe Phe Lys Phe Ala Lys Glu 295 300 305			968
ata tat ccc gga cag ttc cag ccg tct ctg tgt cac aaa ttc ata gct Ile Tyr Pro Gly Gln Phe Gln Pro Ser Leu Cys His Lys Phe Ile Ala 310 315 320			1016
ttg tca gat aag gaa gga aaa cta ctt cga aat tat act caa aat ata Leu Ser Asp Lys Glu Gly Lys Leu Leu Arg Asn Tyr Thr Gln Asn Ile 325 330 335			1064
gat acc ttg gag cag gtt gca gga atc caa agg atc ctt cag tgt cat Asp Thr Leu Glu Gln Val Ala Gly Ile Gln Arg Ile Leu Gln Cys His 340 345 350 355			1112
ggt tcc ttt gca aca gca tct tgc ctg att tgt aaa tac aaa gtt gat Gly Ser Phe Ala Thr Ala Ser Cys Leu Ile Cys Lys Tyr Lys Val Asp 360 365 370			1160
tgt gaa gct gtt cgt gga gac att ttt aat cag gta gtt cct cgg tgc Cys Glu Ala Val Arg Gly Asp Ile Phe Asn Gln Val Val Pro Arg Cys 375 380 385			1208
cct agg tgc cca gct gat gag cca ctt gcc atc atg aag cca gag att Pro Arg Cys Pro Ala Asp Glu Pro Leu Ala Ile Met Lys Pro Glu Ile 390 395 400			1256
gtc ttc ttt ggt gaa aac tta cca gaa cag ttt cat aga gcc atg aag Val Phe Phe Gly Glu Asn Leu Pro Glu Gln Phe His Arg Ala Met Lys 405 410 415			1304
tat gac aaa gat gaa gtt gac ctc ctc att gtt att gga tct tct ctg Tyr Asp Lys Asp Glu Val Asp Leu Leu Ile Val Ile Gly Ser Ser Leu 420 425 430 435			1352
aaa gtg aga cca gta gca cta att cca agt tct ata ccc cat gaa gtg Lys Val Arg Pro Val Ala Leu Ile Pro Ser Ser Ile Pro His Glu Val 440 445 450			1400

cct caa ata tta ata aat agg gaa cct ttg cct cat cta cat ttt gat	1448
Pro Gln Ile Leu Ile Asn Arg Glu Pro Leu Pro His Leu His Phe Asp	
455 460 465	
gta gag ctc ctt gga gac tgc gat gtt ata att aat gag ttg tgt cat	1496
Val Glu Leu Leu Gly Asp Cys Asp Val Ile Ile Asn Glu Leu Cys His	
470 475 480	
agg cta ggt ggt gaa tat gcc aaa ctt tgt tgt aac cct gta aag ctt	1544
Arg Leu Gly Gly Glu Tyr Ala Lys Leu Cys Cys Asn Pro Val Lys Leu	
485 490 495	
tca gaa att act gaa aaa cct cca cgc cca caa aag gaa ttg gtt cat	1592
Ser Glu Ile Thr Glu Lys Pro Pro Arg Pro Gln Lys Glu Leu Val His	
500 505 510 515	
tta tca gag ttg cca cca aca cct ctt cat att tcg gaa gac tca agt	1640
Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu Asp Ser Ser	
520 525 530	
tca cct gaa aga act gta cca caa gac tct tct gtg att gct aca ctt	1688
Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile Ala Thr Leu	
535 540 545	
gta gac caa gca aca aac aac aat gtt aat gat tta gaa gta tct gaa	1736
Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu Val Ser Glu	
550 555 560	
tca agt tgt gtg gaa gaa aaa cca caa gaa gta cag act agt agg aat	1784
Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr Ser Arg Asn	
565 570 575	
gtt gag aac att aat gtg gaa aat cca gat ttt aag gct gtt ggt tcc	1832
Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala Val Gly Ser	
580 585 590 595	
agt act gca gac aaa aat gaa aga act tca gtt gca gaa aca gtg aga	1880
Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu Thr Val Arg	
600 605 610	
aaa tgc tgg cct aat aga ctt gca aag gag cag att agt aag cgg ctt	1928
Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser Lys Arg Leu	
615 620 625	
gag ggt aat caa tac ctg ttt gta cca cca aat cgt tac ata ttc cac	1976
Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr Ile Phe His	
630 635 640	
ggt gct gag gta tac tca gac tct gaa gat gac gtc ttg tcc tct agt	2024
Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu Ser Ser Ser	
645 650 655	
tcc tgt ggc agt aac agt gac agt ggc aca tgc cag agt cca agt tta	2072
Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser Pro Ser Leu	
660 665 670 675	

gaa gaa ccc ttg gaa gat gaa agt gaa att gaa gaa ttc tac aat ggc 2120
 Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe Tyr Asn Gly
 680 685 690

ttg gaa gat gat acg gag agg ccc gaa tgt gct gga gga tct gga ttt 2168
 Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly Ser Gly Phe
 695 700 705

gga gct gat gga ggg gat caa gag gtt gtt aat gaa gct ata gct aca 2216
 Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala Ile Ala Thr
 710 715 720

aga cag gaa ttg aca gat gta aac tat cca tca gac aaa tca 2258
 Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys Ser
 725 730 735

taacactatt gaagctgtcc ggattcagga attgctccac cagcattggg aacttttagca 2318
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 aatactgcca agatgtgaat atgcaaagcc tttctgaatc taataatggg acttctactg 3098
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<210> 26

<211> 737

<212> PRT

<213> Mus musculus

<400> 26

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 Ala Ala Ala Ala Met Glu Ala Ala Ser Gln Pro Ala Asp Glu Pro Leu
 20 25 30
 Arg Lys Arg Pro Arg Arg Asp Gly Pro Gly Leu Gly Arg Ser Pro Gly
 35 40 45
 Glu Pro Ser Ala Ala Val Ala Pro Ala Ala Ala Gly Cys Glu Ala Ala

50	55	60
Ser Ala Ala Ala Pro	Ala Ala Leu Trp Arg	Glu Ala Ala Gly Ala Ala
65	70	75
Ala Ser Ala Glu Arg	Glu Ala Pro Ala Thr	Ala Val Ala Gly Asp Gly
85	90	95
Asp Asn Gly Ser Gly	Leu Arg Arg Glu Pro	Arg Ala Ala Asp Asp Phe
100	105	110
Asp Asp Asp Glu Gly	Glu Glu Glu Asp Glu	Ala Ala Ala Ala Ala Ala
115	120	125
Ala Ala Ala Ile Gly	Tyr Arg Asp Asn Leu	Leu Leu Leu Thr Asp Gly Leu
130	135	140
Leu Thr Asn Gly Phe	His Ser Cys Glu Ser	Asp Asp Asp Asp Arg Thr
145	150	155
Ser His Ala Ser Ser	Ser Asp Trp Thr Pro	Arg Pro Arg Ile Gly Pro
165	170	175
Tyr Thr Phe Val Gln	Gln His Leu Met Ile	Gly Thr Asp Pro Arg Thr
180	185	190
Ile Leu Lys Asp Leu	Leu Pro Glu Thr Ile	Pro Pro Pro Glu Leu Asp
195	200	205
Asp Met Thr Leu Trp	Gln Ile Val Ile Asn	Ile Leu Ser Glu Pro Pro
210	215	220
Lys Arg Lys Lys Arg	Lys Asp Ile Asn Thr	Ile Glu Asp Ala Val Lys
225	230	235
Leu Leu Gln Glu Cys	Lys Lys Ile Ile Val	Leu Thr Gly Ala Gly Val
245	250	255
Ser Val Ser Cys Gly	Ile Pro Asp Phe Arg	Ser Arg Asp Gly Ile Tyr
260	265	270
Ala Arg Leu Ala Val	Asp Phe Pro Asp Leu	Pro Asp Pro Gln Ala Met
275	280	285
Phe Asp Ile Glu Tyr	Phe Arg Lys Asp Pro	Arg Pro Phe Phe Lys Phe
290	295	300
Ala Lys Glu Ile Tyr	Pro Gly Gln Phe Gln	Pro Ser Leu Cys His Lys
305	310	315
Phe Ile Ala Leu Ser	Asp Lys Glu Gly Lys	Leu Leu Arg Asn Tyr Thr
325	330	335
Gln Asn Ile Asp Thr	Leu Glu Gln Val Ala	Gly Ile Gln Arg Ile Leu
340	345	350
Gln Cys His Gly Ser	Phe Ala Thr Ala Ser	Cys Leu Ile Cys Lys Tyr
355	360	365
Lys Val Asp Cys Glu	Ala Val Arg Gly Asp	Ile Phe Asn Gln Val Val
370	375	380
Pro Arg Cys Pro Arg	Cys Pro Ala Asp Glu	Pro Leu Ala Ile Met Lys
385	390	395
Pro Glu Ile Val Phe	Phe Gly Glu Asn Leu	Pro Glu Gln Phe His Arg
405	410	415
Ala Met Lys Tyr Asp	Lys Asp Glu Val Asp	Leu Leu Ile Val Ile Gly
420	425	430
Ser Ser Leu Lys Val	Arg Pro Val Ala Leu	Ile Pro Ser Ser Ile Pro
435	440	445
His Glu Val Pro Gln	Ile Leu Ile Asn Arg	Glu Pro Leu Pro His Leu
450	455	460
His Phe Asp Val Glu	Leu Leu Gly Asp Cys	Asp Val Ile Ile Asn Glu
465	470	475
Leu Cys His Arg Leu	Gly Gly Glu Tyr Ala	Lys Leu Cys Cys Asn Pro
485	490	495
Val Lys Leu Ser Glu	Ile Thr Glu Lys Pro	Pro Arg Pro Gln Lys Glu
500	505	510

Leu Val His Leu Ser Glu Leu Pro Pro Thr Pro Leu His Ile Ser Glu
 515 520 525
 Asp Ser Ser Ser Pro Glu Arg Thr Val Pro Gln Asp Ser Ser Val Ile
 530 535 540
 Ala Thr Leu Val Asp Gln Ala Thr Asn Asn Asn Val Asn Asp Leu Glu
 545 550 555 560
 Val Ser Glu Ser Ser Cys Val Glu Glu Lys Pro Gln Glu Val Gln Thr
 565 570 575
 Ser Arg Asn Val Glu Asn Ile Asn Val Glu Asn Pro Asp Phe Lys Ala
 580 585 590
 Val Gly Ser Ser Thr Ala Asp Lys Asn Glu Arg Thr Ser Val Ala Glu
 595 600 605
 Thr Val Arg Lys Cys Trp Pro Asn Arg Leu Ala Lys Glu Gln Ile Ser
 610 615 620
 Lys Arg Leu Glu Gly Asn Gln Tyr Leu Phe Val Pro Pro Asn Arg Tyr
 625 630 635 640
 Ile Phe His Gly Ala Glu Val Tyr Ser Asp Ser Glu Asp Asp Val Leu
 645 650 655
 Ser Ser Ser Ser Cys Gly Ser Asn Ser Asp Ser Gly Thr Cys Gln Ser
 660 665 670
 Pro Ser Leu Glu Glu Pro Leu Glu Asp Glu Ser Glu Ile Glu Glu Phe
 675 680 685
 Tyr Asn Gly Leu Glu Asp Asp Thr Glu Arg Pro Glu Cys Ala Gly Gly
 690 695 700
 Ser Gly Phe Gly Ala Asp Gly Gly Asp Gln Glu Val Val Asn Glu Ala
 705 710 715 720
 Ile Ala Thr Arg Gln Glu Leu Thr Asp Val Asn Tyr Pro Ser Asp Lys
 725 730 735
 Ser

<210> 27
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<221> VARIANT
 <222> 8
 <223> Xaa = Leu or Ala

<400> 27
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<210> 28
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<400> 28
 Tyr Thr Gln Asn Ile Asp

1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<400> 29
Lys Arg Lys Lys Arg Lys
1 5

<210> 30
<211> 5
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 30
Val Ser Thr Ser Leu
1 5

<210> 31
<211> 5
<212> PRT
<213> *Mus musculus*

<400> 31
Val Ser Val Ser Cys
1 5

<210> 32
<211> 6
<212> PRT
<213> *Mus musculus*

<400> 32
Leu Ile Asn Lys Glu Lys
1 5

<210> 33
<211> 6
<212> PRT
<213> *Mus musculus*

<400> 33
Leu Ile Asn Arg Asp Leu
1 5

<210> 34
<211> 699
<212> DNA
<213> Unknown

<220>
<223> EST cDNA clone 557657

<221> CDS

<222> (3)...(698)

<400> 34

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Thr Arg Pro Arg Thr Arg Gly His Gly Thr Glu Gln Ser Val Thr	
1 5 10 15	
gtc ccg agg gcc ccc acc ccg ttc cca tgg ccg agc cgg acc gat tca	95
Val Pro Arg Ala Pro Thr Pro Phe Pro Trp Pro Ser Arg Thr Asp Ser	
20 25 30	
gac tcg gac act gag gga gga gcc act ggt gga gag gca gag atg gac	143
Asp Ser Asp Thr Glu Gly Gly Ala Thr Gly Gly Glu Ala Glu Met Asp	
35 40 45	
ttc ctg agg aat tta ttc acc cag acc ctg ggc ctg ggt tcc caa aag	191
Phe Leu Arg Asn Leu Phe Thr Gln Thr Leu Gly Leu Gly Ser Gln Lys	
50 55 60	
gag cgt ctt cta gac gag ctg acc ctc gaa gga gtg aca cgc tac atg	239
Glu Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Thr Arg Tyr Met	
65 70 75	
cag agc gag cgc tgc cgc aag gtc atc tgt ttg gtg gga gcc gga atc	287
Gln Ser Glu Arg Cys Arg Lys Val Ile Cys Leu Val Gly Ala Gly Ile	
80 85 90 95	
tcc acg tcc gcg ggt atc cct gac ttc cgc tcc ccg tcc act ggc ctc	335
Ser Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu	
100 105 110	
tat gca aac ctg gag aag tac cac ctt cct tac cca gag gcc atc ttt	383
Tyr Ala Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe	
115 120 125	
gag atc agc tac ttc aag aaa cat ccg gaa ccc ttc ttt gcc ctt gcc	431
Glu Ile Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala Leu Ala	
130 135 140	
aag gag ctc tat ccc ggg cag ttc aag cca acc atc tgc cac tac ttc	479
Lys Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe	
145 150 155	
atc cgc ctg ctg aag gag aag ggg ctg ctg ctg cgc tgc tac acg cag	527
Ile Arg Leu Leu Lys Glu Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln	
160 165 170 175	
aac ata gac acg ctg gaa cga gtg gcg ggg ctg gag ccc cag gac ctg	575
Asn Ile Asp Thr Leu Glu Arg Val Ala Gly Leu Glu Pro Gln Asp Leu	
180 185 190	
gtg gag gcc cac ggc acc ttc tac aca tca cac tgt gtc aac acc tcc	623
Val Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Asn Thr Ser	
195 200 205	

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tgc aga aaa gaa tac acg atg ggc tgg atg aaa gag aag att tct cag 671
Cys Arg Lys Glu Tyr Thr Met Gly Trp Met Lys Glu Lys Ile Ser Gln
      210                215                220

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aag caa ctc cca ggt gtg agc agt gtc a 699
Lys Gln Leu Pro Gly Val Ser Ser Val
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<210> 35
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<213> Unknown

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<220>
<223> EST cDNA clone 557657

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<400> 35
Thr Arg Pro Arg Thr Arg Gly His Gly Thr Glu Gln Ser Val Thr Val
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Pro Arg Ala Pro Thr Pro Phe Pro Trp Pro Ser Arg Thr Asp Ser Asp
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Ser Asp Thr Glu Gly Gly Ala Thr Gly Gly Glu Ala Glu Met Asp Phe
      35              40              45
Leu Arg Asn Leu Phe Thr Gln Thr Leu Gly Leu Gly Ser Gln Lys Glu
      50              55              60
Arg Leu Leu Asp Glu Leu Thr Leu Glu Gly Val Thr Arg Tyr Met Gln
      65              70              75              80
Ser Glu Arg Cys Arg Lys Val Ile Cys Leu Val Gly Ala Gly Ile Ser
      85              90              95
Thr Ser Ala Gly Ile Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr
      100             105             110
Ala Asn Leu Glu Lys Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu
      115             120             125
Ile Ser Tyr Phe Lys Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys
      130             135             140
Glu Leu Tyr Pro Gly Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Ile
      145             150             155             160
Arg Leu Leu Lys Glu Lys Gly Leu Leu Leu Arg Cys Tyr Thr Gln Asn
      165             170             175
Ile Asp Thr Leu Glu Arg Val Ala Gly Leu Glu Pro Gln Asp Leu Val
      180             185             190
Glu Ala His Gly Thr Phe Tyr Thr Ser His Cys Val Asn Thr Ser Cys
      195             200             205
Arg Lys Glu Tyr Thr Met Gly Trp Met Lys Glu Lys Ile Ser Gln Lys
      210             215             220
Gln Leu Pro Gly Val Ser Ser Val
      225             230

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<210> 36
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<212> PRT
<213> Mus musculus

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<400> 36
Thr Leu Gly Leu
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<210> 37
<211> 4
<212> PRT
<213> Mus musculus

<400> 37
Phe Gly Gly Gly
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<210> 38
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> 4
<223> Xaa = Val or Ile

<221> VARIANT
<222> 6
<223> Xaa = Thr or Val

<221> VARIANT
<222> 8
<223> Xaa = Leu, Cys, or Ala

<400> 38
Gly Ala Gly Xaa Ser Xaa Ser Xaa Gly Ile Pro Asp Phe Arg Ser
1 5 10 15